**Amendments to the Specification:**

Please replace page 35, lines 8-10 with the following lines:

practical approach. Schena M. Oxford University Press 1999" and the World Wide Web, ~~(http://cmgm.standford.edu/pbrown/protocols/index.html),~~ ~~http://arrayit.com/DNA-Microarray-Protocols/)~~ and specialized distributors (e.g., Affymetrix).

Please replace page 37, lines 21-24 with the following lines:

The obtained sequence (SEQ ID NO:1) has a putative open reading frame of 259 amino acids (SEQ ID NO:2). The deduced protein sequence was submitted to prediction algorithms for cellular localization using PSORT program and TopPred program. ~~(PSORT: http://psort.nibb.ac.jp/ and TopPred: http//www.biokemi.su.se/~server/toppred2/toppred_source.html~~). It is predicted to have

Please replace page 43, lines 12-22 with the following lines:

The HLA-A2 binding peptide sequences are predicted either by the Parker's algorithm (Parker, K. C., M.A. Bednarek, and J.E. Coligan, 1994. Scheme for ranking potential HLA-A2 binding peptides based on independent binding of individual peptide sidechains. J. Immunol. 152:163 ~~and http://bimas.dcrt.nih.gov/molbio/hla_bind/~~) or the Rammensee method (Rammensee, Friede, Stevanovic, MHC ligands and peptide motifs: 1st listing, Immunogenetics 41, 178-228, 1995; Rammensee, Bachman Stevanovic: MAHC ligand and peptide motifs. Landes Bioscience 1997~~, and http://134.2.96.221/scripts/hlaserver.dll/home.htm~~). Peptides are then screened in the HLA-A2.1/Kb transgenic mice model (Vitiello et al.). The sequence used to perform the prediction is EPHB2v, as it is identical to EPHB2 with an additional C-terminal sequence extension.